

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Malcolm Whitman and Xin Chen
- 5 (ii) TITLE OF THE INVENTION: METHODS AND REAGENTS FOR MODULATING  
TGF-BETA SUPERFAMILY SIGNALLING
- (iii) NUMBER OF SEQUENCES: 18
- (iv) CORRESPONDENCE ADDRESS:
- 10 (A) ADDRESSEE: Clark & Elbing LLP  
(B) STREET: 176 Federal Street  
(C) CITY: Boston  
(D) STATE: MA  
(E) COUNTRY: USA  
(F) ZIP: 02110
- (v) COMPUTER READABLE FORM:
- 15 (A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
- 20 (A) APPLICATION NUMBER:  
(B) FILING DATE: 27-MAY-1998  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- 25 (A) APPLICATION NUMBER: 60/047,991  
(B) FILING DATE: 28-MAY-1997
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Bieker-Brady, Kristina  
(B) REGISTRATION NUMBER: 39,109  
(C) REFERENCE/DOCKET NUMBER: 00246/501002
- 30 (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 617-428-0200  
(B) TELEFAX: 617-428-7045  
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1658 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xenopus Smad2 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGTCGTCCA TCTTGCCTTT CACCCCGCCA GTAGTGAAGC GCCTGCTAGG ATGGAAGAAG 60  
TCTGCAAGTG GCACCACAGG AGCAGGTGGC GATGAGCAGA ACGGACAGGA AGAGAAGTGG 120  
TGCGAAAAAG CGGTAAAGAG CTTGGTGAAA AAAGTGAAGA AAACGGGACA ATTAGACGAG 180  
CTTGAGAAGG CGATCACGAC GCAGAACTGC AACACGAAAT GCGTAACGAT ACCAAGCACT 240  
TGCTCTGAAA TTTGGGGACT GAGTACAGCA AATACCATAG ATCAGTGGGA TACCACAGGC 300  
CTTTACAGCT TCTCTGAACA AACCAGGTCT CTTGATGGTC GACTCCAGGT GTCTCACCGT 360  
AAAGGATTGC CGCATGTTAT CTACTGCAGA CTGTGGCGCT GGCCAGACCT GCACAGTCAT 420  
CATGAACTGA AAGCAATCGA AAATTGTGAA TATGCTTTTA ACCTTAAAAA AGATGAAGTT 480  
TGTGTCAATC CATAACATTA TCAGAGGGTG GAGACACCAG TTTTACCACC TGTATTAGTT 540  
CCACGGCACA CGGAAATCTT GACAGAGCTG CCACCTCTTG ATGACTACAC GCATTCCATT 600  
CCAGAAAACA CTAATTTTCC TGCAGGGATT GAACCTCAGA GCAATTATAT TCCAGAAAACA 660  
CCACCTCCTG GATATATTAG TGAAGATGGA GAAACTAGCG ATCAGCAACT TAACCAAAGC 720  
ATGGACACAG GGTCACCAGC TGAGCTGTCT CCGAGTACAC TTTCTCCAGT CAACCACAAT 780  
CTCGATTGTC AACCTGTCAC CTATTCGGA CCTGCTTTT GGTGCTCTAT AGCATACTAC 840  
GAACTGAATC AGCGAGTAGG AGAAACTTTC CATGCATCGC AACCATCGCT TACCGTGGAC 900  
GGCTTTACGG ACCCCTCAAA CTCTGAAAGG TTCTGCTTAG GTTTACTCTC AAATGTGAAC 960  
CGAAATGCCA CGGTGGAAAT GACCAGGCGT CACATAGGAA GGGGTGTCCG GCTATATTAC 1020  
ATCGGTGGAG AGGTGTTTGC AGAGTGCCTA AGTGATAGTG CTATTTTGTG TCAGAGTCCA 1080  
AACTGTAACC AGCGATATGG ATGGCATCCA GCAACTGTAT GTAAGATTCC TCCAGGATGC 1140  
AATCTGAAGA TTTTCAATAA TCAAGAGTTT GCGGCTCTCC TCGCTCAGTC TGTGAATCAA 1200  
GGCTTTGAAG CAGTTTATCA GTTAACTCGA ATGTGCACCA TAAGGATGAG CTTTGTAATAA 1260  
GGCTGGGGTG CTGAATACAG GCGACAGACC GTTACAAGCA CTCCATGCTG GATTGAGCTT 1320  
CACCTGAATG GACCTTTGCA GTGGTTGGAC AAAGTGTGTA CACAGATGGG ATCCCCTTCA 1380  
GTCCGCTGCT CAAGCATGTC CTAATGGTCT CCTCTTTTTA ATGTATTACC TGCGGGCGGC 1440  
AACTGCAGTC CCAGCAACAG ACTCAATACA GCTTGCTGTG CGTAGTATTT GTGTGTGGTG 1500  
CCCATGAACT GTTTACAATC CAAAAGAGAG AGAATAAAAA AGCAAAAAACA GCACTTGAGA 1560  
TCCCATCAAC GAAAAGCACC TTGTTGGATG ATGTTTCTGA TACTCTTAAA GTAGATCCGT 1620  
GTATAAATGA CTCCTTACCT GGGAAAAGGG ACTTTTTT 1658

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xenopus Smad2

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

	Met	Ser	Ser	Ile	Leu	Pro	Phe	Thr	Pro	Pro	Val	Val	Lys	Arg	Leu	Leu
	1				5				10						15	
5	Gly	Trp	Lys	Lys	Ser	Ala	Ser	Gly	Thr	Thr	Gly	Ala	Gly	Gly	Asp	Glu
				20				25					30			
	Gln	Asn	Gly	Gln	Glu	Glu	Lys	Trp	Cys	Glu	Lys	Ala	Val	Lys	Ser	Leu
			35				40					45				
	Val	Lys	Lys	Leu	Lys	Lys	Thr	Gly	Gln	Leu	Asp	Glu	Leu	Glu	Lys	Ala
	50					55					60					
10	Ile	Thr	Thr	Gln	Asn	Cys	Asn	Thr	Lys	Cys	Val	Thr	Ile	Pro	Ser	Thr
	65				70					75				80		
	Cys	Ser	Glu	Ile	Trp	Gly	Leu	Ser	Thr	Ala	Asn	Thr	Ile	Asp	Gln	Trp
				85					90					95		
	Asp	Thr	Thr	Gly	Leu	Tyr	Ser	Phe	Ser	Glu	Gln	Thr	Arg	Ser	Leu	Asp
15				100					105					110		
	Gly	Arg	Leu	Gln	Val	Ser	His	Arg	Lys	Gly	Leu	Pro	His	Val	Ile	Tyr
			115					120					125			
	Cys	Arg	Leu	Trp	Arg	Trp	Pro	Asp	Leu	His	Ser	His	His	Glu	Leu	Lys
	130						135					140				
20	Ala	Ile	Glu	Asn	Cys	Glu	Tyr	Ala	Phe	Asn	Leu	Lys	Lys	Asp	Glu	Val
	145				150					155				160		
	Cys	Val	Asn	Pro	Tyr	His	Tyr	Gln	Arg	Val	Glu	Thr	Pro	Val	Leu	Pro
				165					170					175		
	Pro	Val	Leu	Val	Pro	Arg	His	Thr	Glu	Ile	Leu	Thr	Glu	Leu	Pro	Pro
25				180					185					190		
	Leu	Asp	Asp	Tyr	Thr	His	Ser	Ile	Pro	Glu	Asn	Thr	Asn	Phe	Pro	Ala
			195				200					205				
	Gly	Ile	Glu	Pro	Gln	Ser	Asn	Tyr	Ile	Pro	Glu	Thr	Pro	Pro	Pro	Gly
	210				215					220						
30	Tyr	Ile	Ser	Glu	Asp	Gly	Glu	Thr	Ser	Asp	Gln	Gln	Leu	Asn	Gln	Ser
	225				230					235				240		
	Met	Asp	Thr	Gly	Ser	Pro	Ala	Glu	Leu	Ser	Pro	Ser	Thr	Leu	Ser	Pro
				245					250					255		
	Val	Asn	His	Asn	Leu	Asp	Leu	Gln	Pro	Val	Thr	Tyr	Ser	Glu	Pro	Ala
35				260					265					270		
	Phe	Trp	Cys	Ser	Ile	Ala	Tyr	Tyr	Glu	Leu	Asn	Gln	Arg	Val	Gly	Glu
			275				280						285			
	Thr	Phe	His	Ala	Ser	Gln	Pro	Ser	Leu	Thr	Val	Asp	Gly	Phe	Thr	Asp
	290					295					300					
40	Pro	Ser	Asn	Ser	Glu	Arg	Phe	Cys	Leu	Gly	Leu	Leu	Ser	Asn	Val	Asn
	305				310					315				320		
	Arg	Asn	Ala	Thr	Val	Glu	Met	Thr	Arg	Arg	His	Ile	Gly	Arg	Gly	Val
				325					330					335		
	Arg	Leu	Tyr	Tyr	Ile	Gly	Gly	Glu	Val	Phe	Ala	Glu	Cys	Leu	Ser	Asp
45				340					345					350		
	Ser	Ala	Ile	Phe	Val	Gln	Ser	Pro	Asn	Cys	Asn	Gln	Arg	Tyr	Gly	Trp
			355				360					365				
	His	Pro	Ala	Thr	Val	Cys	Lys	Ile	Pro	Pro	Gly	Cys	Asn	Leu	Lys	Ile
	370					375						380				
50	Phe	Asn	Asn	Gln	Glu	Phe	Ala	Ala	Leu	Leu	Ala	Gln	Ser	Val	Asn	Gln
	385				390					395					400	
	Gly	Phe	Glu	Ala	Val	Tyr	Gln	Leu	Thr	Arg	Met	Cys	Thr	Ile	Arg	Met
				405					410					415		

Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr  
420 425 430  
Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp  
435 440 445  
5 Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser  
450 455 460  
Ser Met Ser  
465

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xenopus Smad2 MH2 domain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Trp Cys Ser Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr  
1 5 10 15  
Phe His Ala Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp Pro  
20 25 30  
Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg  
35 40 45  
Asn Ala Thr Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val Arg  
50 55 60  
30 Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser  
65 70 75 80  
Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp His  
85 90 95  
35 Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe  
100 105 110  
Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly  
115 120 125  
Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser  
130 135 140  
40 Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser  
145 150 155 160  
Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu  
165 170 175  
45 Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser Ser  
180 185 190  
Met Ser

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1401 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Human Smad2 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGTCGTCCA TCTTGCCATT CACGCCGCCA GTTGTGAAGA GACTGCTGGG ATGGAAGAAG 60  
TCAGCTGGTG GGTCTGGAGG AGCAGGCCGA GGAGAGCAGA ATGGGCAGGA AGAAAAGTGG 120  
TGTGAGAAAG CAGTGAAAAG TCTGGTGAAG AAGCTAAAGA AAACAGGACG ATTAGATGAG 180  
CTTGAGAAAG CCATCACCAC TCAAACTGT AATACTAAAT GTGTTACCAT ACCAAGCACT 240  
TGCTCTGAAA TTTGGGGACT GAGTACACCA AATACGATAG ATCAGTGGGA TACAACAGGC 300  
CTTTACAGCT TCTCTGAACA AACAGGTCT CTTGATGGTC GTCTCCAGGT ATCCCATCGA 360  
AAAGGATTGC CACATGTTAT ATATTGCCGA TTATGGCGCT GGCCTGATCT TCACAGTCAT 420  
CATGAACTCA AGGCAATTGA AAAGTGCAG TATGCTTTTA ATCTTAAAAA GGATGAAGTA 480  
TGTGTAAACC CTTACCACTA TCAGAGAGTT GAGACACCAG TTTTGCCTCC AGTATTAGTG 540  
CCCCGACACA CCGAGATCCT AACAGAACTT CCGCCTCTGG ATGACTATAC TCACTCCATT 600  
CCAGAAAACA CTAAGTCCCT AGCAGGAATT GAGCCACAGA GTAATTATAT TCCAGAAACG 660  
CCACCTCTCG GATATATCAG TGAAGATGGA GAAACAAGTG ACCAACAGTT GAATCAAAGT 720  
ATGGACACAG GCTCTCCAGC AGAAGTATCT CCTACTACTC TTTCCCTGT TAATCATAGC 780  
TTGGATTAC AGCCAGTTAC TTACTCAGAA CCTGCATTTT GGTGTTCAAT AGCATATTAT 840  
GAATTAAATC AGAGGGTTGG AGAAACCTTC CATGCATCAC AGCCCTCACT CACTGTAGAT 900  
GGCTTTACAG ACCCATCAAA TTCAGAGAGG TTCTGCTTAG GTTTACTCTC CAATGTTAAC 960  
CGAAATGCCA CGGTAGAAAT GACAAGAAGG CATATAGGAA GAGGAGTGCG CTTATACTAC 1020  
ATAGGTGGGG AAGTTTTTGC TGAGTGCCTA AGTGATAGTG CAATCTTTGT GCAGAGCCCC 1080  
AATTGTAATC AGAGATATGG CTGGCACCTT GCAACAGTGT GTAAAATTCC ACCAGGCTGT 1140  
AATCTGAAGA TCTTCAACAA CCAGGAATTT GCTGCTCTTC TGGCTCAGTC TGTTAATCAG 1200  
GGTTTTGAAG CCGTCTATCA GCTAACTAGA ATGTGCACCA TAAGAATGAG TTTTGTGAAA 1260  
GGGTGGGGAG CAGAATACCG AAGGCAGACG GTAACAAGTA CTCCTTGCTG GATTGAACTT 1320  
CATCTGAATG GACCTCTACA GTGGTTGGAC AAAGTATTAA CTCAGATGGG ATCCCCTTCA 1380  
GTGCGTTGCT CAAGCATGTC A 1401

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Human Smad2

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	Met	Ser	Ser	Ile	Leu	Pro	Phe	Thr	Pro	Pro	Val	Val	Lys	Arg	Leu	Leu
	1				5					10					15	
	Gly	Trp	Lys	Lys	Ser	Ala	Gly	Gly	Ser	Gly	Gly	Ala	Gly	Gly	Gly	Glu
			20						25					30		
10	Gln	Asn	Gly	Gln	Glu	Glu	Lys	Trp	Cys	Glu	Lys	Ala	Val	Lys	Ser	Leu
		35					40						45			
	Val	Lys	Lys	Leu	Lys	Lys	Thr	Gly	Arg	Leu	Asp	Glu	Leu	Glu	Lys	Ala
	50					55					60					
15	Ile	Thr	Thr	Gln	Asn	Cys	Asn	Thr	Lys	Cys	Val	Thr	Ile	Pro	Ser	Thr
	65				70					75				80		
	Cys	Ser	Glu	Ile	Trp	Gly	Leu	Ser	Thr	Pro	Asn	Thr	Ile	Asp	Gln	Trp
				85					90					95		
	Asp	Thr	Thr	Gly	Leu	Tyr	Ser	Phe	Ser	Glu	Gln	Thr	Arg	Ser	Leu	Asp
				100				105					110			
20	Gly	Arg	Leu	Gln	Val	Ser	His	Arg	Lys	Gly	Leu	Pro	His	Val	Ile	Tyr
		115					120					125				
	Cys	Arg	Leu	Trp	Arg	Trp	Pro	Asp	Leu	His	Ser	His	His	Glu	Leu	Lys
		130					135				140					
25	Ala	Ile	Glu	Asn	Cys	Glu	Tyr	Ala	Phe	Asn	Leu	Lys	Lys	Asp	Glu	Val
	145				150					155				160		
	Cys	Val	Asn	Pro	Tyr	His	Tyr	Gln	Arg	Val	Glu	Thr	Pro	Val	Leu	Pro
				165					170					175		
	Pro	Val	Leu	Val	Pro	Arg	His	Thr	Glu	Ile	Leu	Thr	Glu	Leu	Pro	Pro
			180					185					190			
30	Leu	Asp	Asp	Tyr	Thr	His	Ser	Ile	Pro	Glu	Asn	Thr	Asn	Phe	Pro	Ala
		195					200					205				
	Gly	Ile	Glu	Pro	Gln	Ser	Asn	Tyr	Ile	Pro	Glu	Thr	Pro	Pro	Pro	Gly
		210					215					220				
35	Tyr	Ile	Ser	Glu	Asp	Gly	Glu	Thr	Ser	Asp	Gln	Gln	Leu	Asn	Gln	Ser
	225				230					235				240		
	Met	Asp	Thr	Gly	Ser	Pro	Ala	Glu	Leu	Ser	Pro	Thr	Thr	Leu	Ser	Pro
				245					250					255		
	Val	Asn	His	Ser	Leu	Asp	Leu	Gln	Pro	Val	Thr	Tyr	Ser	Glu	Pro	Ala
			260					265					270			
40	Phe	Trp	Cys	Ser	Ile	Ala	Tyr	Tyr	Glu	Leu	Asn	Gln	Arg	Val	Gly	Glu
		275					280					285				
	Thr	Phe	His	Ala	Ser	Gln	Pro	Ser	Leu	Thr	Val	Asp	Gly	Phe	Thr	Asp
		290					295					300				
45	Pro	Ser	Asn	Ser	Glu	Arg	Phe	Cys	Leu	Gly	Leu	Leu	Ser	Asn	Val	Asn
	305				310					315				320		
	Arg	Asn	Ala	Thr	Val	Glu	Met	Thr	Arg	Arg	His	Ile	Gly	Arg	Gly	Val
				325					330				335			
	Arg	Leu	Tyr	Tyr	Ile	Gly	Gly	Glu	Val	Phe	Ala	Glu	Cys	Leu	Ser	Asp
			340				345					350				
50	Ser	Ala	Ile	Phe	Val	Gln	Ser	Pro	Asn	Cys	Asn	Gln	Arg	Tyr	Gly	Trp
		355					360					365				
	His	Pro	Ala	Thr	Val	Cys	Lys	Ile	Pro	Pro	Gly	Cys	Asn	Leu	Lys	Ile

370 375 380  
 Phe Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln  
 385 390 395 400  
 Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met  
 405 410 415  
 Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr  
 420 425 430  
 Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp  
 435 440 445  
 10 Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser  
 450 455 460  
 Ser Met Ser  
 465

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Human Smad2 MH2 domain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Trp Cys Ser Ile Ala Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr  
 1 5 10 15  
 Phe His Ala Ser Gln Pro Ser Leu Thr Val Asp Gly Phe Thr Asp Pro  
 20 25 30  
 Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg  
 35 40 45  
 Asn Ala Thr Val Glu Met Thr Arg Arg His Ile Gly Arg Gly Val Arg  
 50 55 60  
 35 Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser  
 65 70 75 80  
 Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp His  
 85 90 95  
 Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe  
 100 105 110  
 Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly  
 115 120 125  
 Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser  
 130 135 140  
 45 Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser  
 145 150 155 160  
 Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu  
 165 170 175

Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Val Arg Cys Ser Ser  
 180 185 190  
 Met Ser

5 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2234 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...1272  
 (D) OTHER INFORMATION:

- (A) NAME/KEY: Other  
 (B) LOCATION: 1...1  
 (D) OTHER INFORMATION: Human Smad3 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG TCG TCC ATC CTG CCT TTC ACT CCC CCG ATC GTG AAG CGC CTG CTG	48
Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Ile Val Lys Arg Leu Leu	
1 5 10 15	
GGC TGG AAG AAG GGC GAG CAG AAC GGG CAG GAG GAG AAA TGG TGC GAG	96
Gly Trp Lys Lys Gly Glu Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu	
20 25 30	
AAG GCG GTC AAG AGC CTG GTC AAG AAA CTC AAG AAG ACG GGG CAG CTG	144
Lys Ala Val Lys Ser Leu Val Lys Lys Leu Lys Lys Thr Gly Gln Leu	
35 40 45	
GAC GAG CTG GAG AAG GCC ATC ACC ACG CAG AAC GTC AAC ACC AAG TGC	192
Asp Glu Leu Glu Lys Ala Ile Thr Thr Gln Asn Val Asn Thr Lys Cys	
50 55 60	
ATC ACC ATC CCC AGG TCC CTG GAT GGC CGG TTG CAG GTG TCC CAT CGG	240
Ile Thr Ile Pro Arg Ser Leu Asp Gly Arg Leu Gln Val Ser His Arg	
65 70 75 80	
AAG GGG CTC CCT CAT GTC ATC TAC TGC CCT GTG CCA TGG CCA GAC CTG	288
Lys Gly Leu Pro His Val Ile Tyr Cys Pro Val Arg Trp Pro Asp Leu	
85 90 95	
CAC AGC CAC CAC GAG CTG CGG GCC ATG GAG CTG TGT GAG TTC GCC TTC	336
His Ser His His Glu Leu Arg Ala Met Glu Leu Cys Glu Phe Ala Phe	



5  
10  
15  
20  
25  
30  
35  
40

- 61 -

	CAG CGC TAT GGC TGG CAC CCG GCC ACC GTC TGC AAG ATC CCA CCA GGA	1008
	Gln Arg Tyr Gly Trp His Pro Ala Thr Val Cys Lys Ile Pro Pro Gly	
	325 330 335	
5	TGC AAC CTG AAG ATC TTC AAC AAC CAG GAG TTC GCT GCC CTC CTG GCC	1056
	Cys Asn Leu Lys Ile Phe Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala	
	340 345 350	
	CAG TCG GTC AAC CAG GGC TTT GAG GCT GTC TAC CAG TTG ACC CGA ATG	1104
	Gln Ser Val Asn Gln Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg Met	
	355 360 365	
10	TGC ACC ATC CGC ATG AGC TTC GTC AAA GGC TGG GGA GCG GAG TAC AGG	1152
	Cys Thr Ile Arg Met Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg	
	370 375 380	
	AGA CAG ACT GTG ACC AGT ACC CCC TGC TGG ATT GAG CTG CAC CTG AAT	1200
	Arg Gln Thr Val Thr Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn	
15	385 390 395 400	
	GGG CCT TTG CAG TGG CTT GAC AAG GTC CTC ACC CAG ATG GGC TCC CCA	1248
	Gly Pro Leu Gln Trp Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro	
	405 410 415	
20	AGC ATC CGC TGT TCC AGT GTG TCT TAGAGACATC AAGTATGGTA GGGGAGGGCA	1302
	Ser Ile Arg Cys Ser Ser Val Ser	
	420	
	GGCTTGGGGA AAATGGCCAT ACAGGAGGTG GAGAAAATTG GAACTCTACT CAACCCATTG	1362
	TTGTCAAGGA AGAAGAAATC TTTCTCCCTC AACTGAAGGG GTGCACCCAC CTGTTTTCTG	1422
	AAACACACGA GCAAACCCAG AGGTGGATGT TATGAACAGC TGTGTCTGCC AAACACATTT	1482
25	ACCTTTTGGC CCCACTTTGA AGGGCAAGAA ATGGCGTCTG CTCTGGTGGC TTAAGTGAGC	1542
	AGAACAGGTA GTATTACACC ACCGGCACCC TCCCCCAGA CTCTTTTTTT GAGTGACAGC	1602
	TTTCTGGGAT GTCACAGTCC AACCAGAAAG GCCCCTCTGT CTAGGACTGC AGTGTGGAGT	1662
	TCACCTTGGA AGGGCGTTCT AGGTAGGAAG AGCCCGCACG ATGCAGACCT CATGCCCAGC	1722
	TCTCTGACGC TTGTGACAGT GCCTCTTCCA GTGAACATT CAGCCCAGC CCCGCCCCGT	1782
30	TGTGAGCTGG ATAGACTTGG GATGGGGAGG GAGGGAGTTT TGTCTGTCTC CCTCCCCCT	1842
	CAGAACATAC TGATTGGGAG GTGCGTGTTC AGCAGAACCT GCACACAGGA CAGCGGGAAA	1902
	AATCGATGAG CGCCACCTCT TTA AAAACTC ACTTACGTTG TCCTTTTTTCA CTTTGAAAAG	1962
	TTGGAAGGAC TGCTGAGGCC CAGTGCATAT GCAATGTATA GTGTCTATTA TCACATTAAT	2022
	CTCAAAGAGA TTCGAATGAC GGTAAGTGT CTATGAAGC AGGAGGCCCT TGTCGTGGGA	2082
35	TGGCATTTGG TCTCAGGCAG CACCACACTG GGTGCGTCTC CAGTCATCTG TAAGAGCTTG	2142
	CTCCAGATTC TGATGCATAC GGCTATATTG GTTTATGTAG TCAGTTGCAT TCATTAAATC	2202
	AACTTTATCA TATGCTCAAA AAAAAAAAAA AG	2234

(2) INFORMATION FOR SEQ ID NO:8:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 424 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Human Smad3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Ser Ile Leu Pro Phe Thr Pro Pro Ile Val Lys Arg Leu Leu  
1 5 10 15  
Gly Trp Lys Lys Gly Glu Gln Asn Gly Gln Glu Glu Lys Trp Cys Glu  
20 25 30  
Lys Ala Val Lys Ser Leu Val Lys Lys Leu Lys Lys Thr Gly Gln Leu  
35 40 45  
Asp Glu Leu Glu Lys Ala Ile Thr Thr Gln Asn Val Asn Thr Lys Cys  
50 55 60  
Ile Thr Ile Pro Arg Ser Leu Asp Gly Arg Leu Gln Val Ser His Arg  
65 70 75 80  
Lys Gly Leu Pro His Val Ile Tyr Cys Pro Val Arg Trp Pro Asp Leu  
85 90 95  
His Ser His His Glu Leu Arg Ala Met Glu Leu Cys Glu Phe Ala Phe  
100 105 110  
Asn Met Lys Lys Asp Glu Val Cys Val Asn Pro Tyr His Tyr Gln Arg  
115 120 125  
Val Glu Thr Pro Val Leu Pro Pro Val Leu Val Pro Arg His Thr Glu  
130 135 140  
Ile Pro Ala Glu Phe Pro Pro Leu Asp Asp Tyr Ser His Ser Ile Pro  
145 150 155 160  
Glu Asn Thr Asn Phe Pro Ala Gly Ile Glu Pro Gln Ser Asn Ile Pro  
165 170 175  
Glu Thr Pro Pro Pro Gly Tyr Leu Ser Glu Asp Gly Glu Thr Ser Asp  
180 185 190  
His Gln Met Asn His Ser Met Asp Ala Gly Ser Pro Asn Leu Ser Pro  
195 200 205  
Asn Pro Met Ser Pro Ala His Asn Asn Leu Asp Leu Gln Pro Val Thr  
210 215 220  
Tyr Cys Glu Pro Ala Phe Trp Cys Ser Ile Ser Tyr Tyr Glu Leu Asn  
225 230 235 240  
Gln Arg Val Gly Glu Thr Phe His Ala Ser Gln Pro Ser Met Thr Val  
245 250 255  
Asp Gly Phe Thr Asp Pro Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu  
260 265 270  
Leu Ser Asn Val Asn Arg Asn Ala Val Glu Leu Thr Arg Arg His  
275 280 285  
Ile Gly Arg Gly Val Arg Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala  
290 295 300  
Glu Cys Leu Ser Asp Ser Ala Ile Phe Val Gln Ser Pro Asn Cys Asn  
305 310 315 320  
Gln Arg Tyr Gly Trp His Pro Ala Thr Val Cys Lys Ile Pro Pro Gly  
325 330 335  
Cys Asn Leu Lys Ile Phe Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala  
340 345 350  
Gln Ser Val Asn Gln Gly Phe Glu Ala Val Tyr Gln Leu Thr Arg Met

355                      360                      365  
 Cys Thr Ile Arg Met Ser Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg  
 370                      375                      380  
 Arg Gln Thr Val Thr Ser Thr Pro Cys Trp Ile Glu Leu His Leu Asn  
 385                      390                      395                      400  
 Gly Pro Leu Gln Trp Leu Asp Lys Val Leu Thr Gln Met Gly Ser Pro  
 405                      410                      415  
 Ser Ile Arg Cys Ser Ser Val Ser  
 420

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Human Smad3 MH2 domain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Trp Cys Ser Ile Ser Tyr Tyr Glu Leu Asn Gln Arg Val Gly Glu Thr  
 1                      5                      10                      15  
 Phe His Ala Ser Gln Pro Ser Met Thr Val Asp Gly Phe Thr Asp Pro  
 20                      25                      30  
 Ser Asn Ser Glu Arg Phe Cys Leu Gly Leu Leu Ser Asn Val Asn Arg  
 35                      40                      45  
 Asn Ala Ala Val Glu Leu Thr Arg Arg His Ile Gly Arg Gly Val Arg  
 50                      55                      60  
 Leu Tyr Tyr Ile Gly Gly Glu Val Phe Ala Glu Cys Leu Ser Asp Ser  
 65                      70                      75                      80  
 Ala Ile Phe Val Gln Ser Pro Asn Cys Asn Gln Arg Tyr Gly Trp His  
 85                      90                      95  
 Pro Ala Thr Val Cys Lys Ile Pro Pro Gly Cys Asn Leu Lys Ile Phe  
 100                      105                      110  
 Asn Asn Gln Glu Phe Ala Ala Leu Leu Ala Gln Ser Val Asn Gln Gly  
 115                      120                      125  
 Phe Glu Ala Val Tyr Gln Leu Thr Arg Met Cys Thr Ile Arg Met Ser  
 130                      135                      140  
 Phe Val Lys Gly Trp Gly Ala Glu Tyr Arg Arg Gln Thr Val Thr Ser  
 145                      150                      155                      160  
 Thr Pro Cys Trp Ile Glu Leu His Leu Asn Gly Pro Leu Gln Trp Leu  
 165                      170                      175  
 Asp Lys Val Leu Thr Gln Met Gly Ser Pro Ser Ile Arg Cys Ser Ser  
 180                      185                      190  
 Val Ser

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1605 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence  
(B) LOCATION: 1...1554  
(D) OTHER INFORMATION:

- (A) NAME/KEY: Other

- (B) LOCATION: 1...1

- (D) OTHER INFORMATION: Xenopus FAST-1 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG AGA GAC CCC TCC AGT CTG TAC TCA GGA TTC CCA GCT GGA TCC CAG	48
Met Arg Asp Pro Ser Ser Leu Tyr Ser Gly Phe Pro Ala Gly Ser Gln	
1 5 10 15	
TAT GAA AGT GTG GAG CCT CCC AGC CTT GCC CTG CTG AGC TCT ATA GAC	96
Tyr Glu Ser Val Glu Pro Pro Ser Leu Ala Leu Leu Ser Ser Ile Asp	
20 25 30	
CAG GAG CAG CTC CCA GTG GCC ACC GGC CAG TCC TAT AAT CAC AGT GTC	144
Gln Glu Gln Leu Pro Val Ala Thr Gly Gln Ser Tyr Asn His Ser Val	
35 40 45	
CAG CCT TGG CCC CAA CCT TGG CCA CCC TTG TCC CTG TAC AGA GAG GGG	192
Gln Pro Trp Pro Gln Pro Trp Pro Pro Leu Ser Leu Tyr Arg Glu Gly	
50 55 60	
GGC ACG TGG AGC CCA GAC AGA GGC AGT ATG TAT GGA CTC TCC CCC GGC	240
Gly Thr Trp Ser Pro Asp Arg Gly Ser Met Tyr Gly Leu Ser Pro Gly	
65 70 75 80	
ACC CAC GAG GGC TCC TGC ACC CAC ACT CAC GAG GGC CCC AAG GAC TCA	288
Thr His Glu Gly Ser Cys Thr His Thr His Glu Gly Pro Lys Asp Ser	
85 90 95	
ATG GCA GGA GAC CAG ACC AGG TCC AGG AAG AGC AAA AAG AAG AAT TAT	336
Met Ala Gly Asp Gln Thr Arg Ser Arg Lys Ser Lys Lys Lys Asn Tyr	
100 105 110	
CAT CGA TAT AAC AAG CCC CCC TAT TCC TAC CTG GCT ATG ATT GCC CTG	384
His Arg Tyr Asn Lys Pro Pro Tyr Ser Tyr Leu Ala Met Ile Ala Leu	
115 120 125	

	GTC ATC CAG AAC TCG CCC GAG AAG AGG CTC AAA CTC TCC CAG ATC CTG	432
	Val Ile Gln Asn Ser Pro Glu Lys Arg Leu Lys Leu Ser Gln Ile Leu	
	130 135 140	
5	AAG GAG GTC AGT ACA CTC TTC CCC TTC TTT AAT GGG GAT TAT ATG GGT	480
	Lys Glu Val Ser Thr Leu Phe Pro Phe Phe Asn Gly Asp Tyr Met Gly	
	145 150 155 160	
	TGG AAA GAC TCC ATC AGG CAC AAC TTG TCT TCC AGT GAC TGC TTT AAG	528
	Trp Lys Asp Ser Ile Arg His Asn Leu Ser Ser Ser Asp Cys Phe Lys	
	165 170 175	
10	AAG ATT CTC AAA GAC CCT GGA AAG CCC CAG GCC AAG GGT AAC TTC TGG	576
	Lys Ile Leu Lys Asp Pro Gly Lys Pro Gln Ala Lys Gly Asn Phe Trp	
	180 185 190	
15	ACG GTG GAT GTT AGC CGG ATT CCT CTG GAT GCG ATG AAG CTG CAG AAC	624
	Thr Val Asp Val Ser Arg Ile Pro Leu Asp Ala Met Lys Leu Gln Asn	
	195 200 205	
	ACT GCG TTG ACC CGA GGT GGA TCA GAC TAC TTT GTC CAG GAT TTG GCT	672
	Thr Ala Leu Thr Arg Gly Gly Ser Asp Tyr Phe Val Gln Asp Leu Ala	
	210 215 220	
20	CCA TAC ATC CTA CAT AAC TAT AAA TAT GAG CAC AAT GCA GGG GCG TAT	720
	Pro Tyr Ile Leu His Asn Tyr Lys Tyr Glu His Asn Ala Gly Ala Tyr	
	225 230 235 240	
	GGT CAC CAG ATG CCT CCA AGT CAT GCC AGA TCC CTG TCT TTG GCA GAG	768
	Gly His Gln Met Pro Pro Ser His Ala Arg Ser Leu Ser Leu Ala Glu	
	245 250 255	
25	GAC TCT CAA CAG ACC AAC ACT GGT GGC AAA CTT AAC ACA TCC TTT ATG	816
	Asp Ser Gln Gln Thr Asn Thr Gly Gly Lys Leu Asn Thr Ser Phe Met	
	260 265 270	
30	ATT GAT TCC CTA CTC CAT GAC CTG CAA GAG GTG GAT CTG CCT GAT GCC	864
	Ile Asp Ser Leu Leu His Asp Leu Gln Glu Val Asp Leu Pro Asp Ala	
	275 280 285	
	TCC AGG AAC CTT GAG AAC CAA AGG ATC TCT CCG GCT GTA GCC ATG AAC	912
	Ser Arg Asn Leu Glu Asn Gln Arg Ile Ser Pro Ala Val Ala Met Asn	
	290 295 300	
35	AAT ATG TGG AGC TCT GCT CCT CTT CTC TAC ACT CAT TCC AAG CCA ACA	960
	Asn Met Trp Ser Ser Ala Pro Leu Leu Tyr Thr His Ser Lys Pro Thr	
	305 310 315 320	
	AGG AAT GCC AGA AGC CCT GGT TTG TCC ACC ATC CAT TCC ACG TAC TCC	1008
	Arg Asn Ala Arg Ser Pro Gly Leu Ser Thr Ile His Ser Thr Tyr Ser	
	325 330 335	
40	TCT TCC AGC TCC AGC ATT TCT ACA ATC TCC CCC GTT GGG TTT CAG AAG	1056
	Ser Ser Ser Ser Ser Ile Ser Thr Ile Ser Pro Val Gly Phe Gln Lys	

[illegible]

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 534 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...1

(D) OTHER INFORMATION: Xenopus FAST-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Arg Asp Pro Ser Ser Leu Tyr Ser Gly Phe Pro Ala Gly Ser Gln  
1 5 10 15  
Tyr Glu Ser Val Glu Pro Pro Ser Leu Ala Leu Leu Ser Ser Ile Asp  
20 25 30  
Gln Glu Gln Leu Pro Val Ala Thr Gly Gln Ser Tyr Asn His Ser Val  
35 40 45  
Gln Pro Trp Pro Gln Pro Trp Pro Pro Leu Ser Leu Tyr Arg Glu Gly  
50 55 60  
Gly Thr Trp Ser Pro Asp Arg Gly Ser Met Tyr Gly Leu Ser Pro Gly  
65 70 75 80  
Thr His Glu Gly Ser Cys Thr His Thr His Glu Gly Pro Lys Asp Ser  
85 90 95  
Met Ala Gly Asp Gln Thr Arg Ser Arg Lys Ser Lys Lys Asn Tyr  
100 105 110  
His Arg Tyr Asn Lys Pro Pro Tyr Ser Tyr Leu Ala Met Ile Ala Leu  
115 120 125  
Val Ile Gln Asn Ser Pro Glu Lys Arg Leu Lys Leu Ser Gln Ile Leu  
130 135 140  
Lys Glu Val Ser Thr Leu Phe Pro Phe Phe Asn Gly Asp Tyr Met Gly  
145 150 155 160  
Trp Lys Asp Ser Ile Arg His Asn Leu Ser Ser Ser Asp Cys Phe Lys  
165 170 175  
Lys Ile Leu Lys Asp Pro Gly Lys Pro Gln Ala Lys Gly Asn Phe Trp  
180 185 190  
Thr Val Asp Val Ser Arg Ile Pro Leu Asp Ala Met Lys Leu Gln Asn  
195 200 205  
Thr Ala Leu Thr Arg Gly Gly Ser Asp Tyr Phe Val Gln Asp Leu Ala  
210 215 220  
Pro Tyr Ile Leu His Asn Tyr Lys Tyr Glu His Asn Ala Gly Ala Tyr  
225 230 235 240  
Gly His Gln Met Pro Pro Ser His Ala Arg Ser Leu Ser Leu Ala Glu  
245 250 255  
Asp Ser Gln Gln Thr Asn Thr Gly Gly Lys Leu Asn Thr Ser Phe Met  
260 265 270  
Ile Asp Ser Leu Leu His Asp Leu Gln Glu Val Asp Leu Pro Asp Ala  
275 280 285  
Ser Arg Asn Leu Glu Asn Gln Arg Ile Ser Pro Ala Val Ala Met Asn  
290 295 300  
Asn Met Trp Ser Ser Ala Pro Leu Leu Tyr Thr His Ser Lys Pro Thr  
305 310 315 320  
Arg Asn Ala Arg Ser Pro Gly Leu Ser Thr Ile His Ser Thr Tyr Ser  
325 330 335



Ser Ser Ser Ser Ser Ile Ser Thr Ile Ser Pro Val Gly Phe Gln Lys  
340 345 350  
Glu Gln Glu Lys Ser Gly Arg Gln Thr Gln Arg Val Gly His Pro Ile  
355 360 365  
5 Lys Arg Ser Arg Glu Asp Asp Asp Cys Ser Thr Thr Ser Ser Asp Pro  
370 375 380  
Asp Thr Gly Asn Tyr Ser Pro Ile Glu Pro Pro Lys Lys Met Pro Leu  
385 390 395 400  
10 Leu Ser Leu Asp Leu Pro Thr Ser Tyr Thr Lys Ser Val Ala Pro Asn  
405 410 415  
Val Val Ala Pro Pro Ser Val Leu Pro Phe Phe His Phe Pro Arg Phe  
420 425 430  
Thr Tyr Tyr Asn Tyr Gly Pro Ser Pro Tyr Met Thr Pro Pro Tyr Trp  
435 440 445  
15 Gly Phe Pro His Pro Thr Asn Ser Gly Gly Asp Ser Pro Arg Gly Pro  
450 455 460  
Gln Ser Pro Leu Asp Leu Asp Asn Met Leu Arg Ala Met Pro Pro Asn  
465 470 475 480  
20 Lys Ser Val Phe Asp Val Leu Thr Ser His Pro Gly Asp Leu Val His  
485 490 495  
Pro Ser Phe Leu Ser Gln Cys Leu Gly Ser Ser Gly Ser Pro Tyr Pro  
500 505 510  
Ser Arg Gln Gly Leu Met Tyr Arg Arg Arg Pro Pro Gly Leu Thr Trp  
515 520 525  
25 Ser Gly His Ser Met Lys  
530

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Xenopus FAST-1 SID

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Thr Ser Ser Asp Pro Asp Thr Gly Asn Tyr Ser Pro Ile Glu Pro Pro  
1 5 10 15  
Lys Lys Met Pro Leu Leu Ser Leu Asp Leu Pro Thr Ser Tyr Thr Lys  
20 25 30  
Ser Val Ala Pro Asn Val Val Ala Pro Pro Ser Val Leu Pro Phe Phe  
35 40 45  
45 His Phe Pro Arg Phe Thr Tyr Tyr Asn Tyr Gly Pro Ser Pro Tyr Met  
50 55 60  
Thr Pro Pro Tyr Trp Gly Phe Pro His Pro Thr Asn Ser Gly Gly Asp  
65 70 75 80

Ser Pro Arg Gly Pro Gln Ser Pro Leu Asp Leu Asp Asn Met Leu Arg  
85 90 95  
Ala Met Pro Pro Asn Lys Ser Val Phe Asp Val Leu Thr Ser His Pro  
100 105 110  
5 Gly Asp Leu Val His Pro Ser Phe Leu Ser Gln Cys Leu Gly Ser Ser  
115 120 125  
Gly Ser Pro Tyr Pro Ser Arg Gln Gly Leu Met Tyr Arg Arg Arg Pro  
130 135 140  
10 Pro Gly Leu Thr Trp Ser Gly His Ser Met Lys  
145 150 155

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1634 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Human FAST-1 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATGGGGCCCT GCAGCGGCTC CCGCCTGGGG CCCCCAGAGG CTGAGTCGCC CTCCCAGCCC 60  
CCTAAGAGGA GGAAGAAGAG GTACCTGCGA CATGACAAGC CCCCCTACAC CTACTTGGCC 120  
ATGATCGCCT TGGTGATTCA GGCCGCTCCC TCCCGCAGAC TGAAGCTGGC CCAGATCATC 180  
CGTCAGGTCC AGGCCGTGTT CCCCTTCTTC AGGGAAGACT ACGAGGGCTG GAAAGACTCC 240  
ATTCGCCACA ACCTTTCTCT CAACCGATGC TTCCGCAAGG TGCCCAAGGA CCCTGCAAAG 300  
CCCCAGGCCA AGGGCAACTT CTGGGCGGTC GACGTGAGCC TGATCCCAGC TGAGGCGCTC 360  
CGGCTGCAGA ACACCGCCCT GTGCCGGCGC TGGCAGAACG GAGGTGCGCG TGGAGCCTTC 420  
GCCAAGGACC TGGGCCCCCTA CGTGCTGCAC GGCCGGCCAT ACCGGCCGCC CAGTCCCCCG 480  
CCACCACCCA GTGAGGGCTT CAGCATCAAG TCCCTGCTAA GAAGGTCCGG GGAAGGGGCA 540  
CCCTGGCCGG GGCTAGCTCC ACAGAACAGC CCAGTTCCTG CAGGCACAGG GAACAATGGG 600  
GAAGAAGCGG TGCCCACCCC ACCCCTTCCC TCTTCTGAAA GGCTCTGTG GCCCCTCTGC 660  
35 CCCCTTCCTG GCCCCACGAG AGTGGAGGGG GAGACTGTGC AGGGGGGAGC CATGGGCCCT 720  
CAACCCTCTC CCCAGAGCCT AGGGCCTGGC CTTTCCACTA CTGCAGGGCA CCGCAGTTCT 780  
GGGGGACGGT CCAGCGGGGG ACACAGGGCC TCCCTTTGGG GGCAGCTGCC CACCTCCTAC 840  
TTGCCTATCT ACACTCCCAA TGTGGTAATG CCCTTGGCAC CACCACCCAC CTCCTGTCCC 900  
CAGTGTCGGT CAACCAGCCC TGCCTACTGG GGGGTGGCCC CTGAAACCCG AGGGCCCCCA 960  
40 GGGCTGCTCT GCGATCTAAA CGCCTCTTC CAAGGGGTGC CACCCAACAA AAGCATCTAC 1020  
GACGTTTGGG TCAGCCACCC TCGGGACCTG GCGGCCCTG GCCCAGGCTG GCTGCTCTCC 1080  
TGGTGCAGCC TGTGAGGCTC TTAAGACAGG GGCCGCTCCT CCCTCCCGCT CCCACCCCA 1140  
CCTTGTTGAC AGGGAGCCAA GGCGAGGCGG CTGTCTGCGA CACAGCAGC CTCGAAACAC 1200  
CAGGCAGCAG CCTTGCTGGG AGTCCACGGT GTTTATTGGG CCACCCACG CATGGCCGTG 1260  
45 GCCCAGCTGG GCACAACCCT CACCCTGGTC TGTCAATGCT GTTTTCTCTA CACTCAGCGG 1320  
CAAACTGCA GGAGCAGGCT GAACCTGAAT ATCCCTCTT AATCCCTCTT CTCAGCCAC 1380  
TACCATCCA TCAGTCACCA GCGTCACCT CCTCCCGTG CTCCAGCTGG GGAAGGAAA 1440  
ACCATGTGG ATCACCCTGAA ATCCTGCCCT CTCTCTCTGT CGGAAAAGAA GTCCACCTTT 1500

TTCCGGAAC CGGTTAGGGA ATTAAATGC CCTACATGTC CTGGTGGTTG GGGGGGAAAC 1560  
 CACTAAAGGA ATTTGCAACC TTTTATCC TCTTCATTT ATCCCAAGGG GGGGCCCGTC 1620  
 CCATTTCCCC AACC 1634

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Human FAST-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Gly	Pro	Cys	Ser	Gly	Ser	Arg	Leu	Gly	Pro	Pro	Glu	Ala	Glu	Ser	1	5	10	15
Pro	Ser	Gln	Pro	Pro	Lys	Arg	Arg	Lys	Lys	Arg	Tyr	Leu	Arg	His	Asp	20	25	30	
Lys	Pro	Pro	Tyr	Thr	Tyr	Leu	Ala	Met	Ile	Ala	Leu	Val	Ile	Gln	Ala	35	40	45	
Ala	Pro	Ser	Arg	Arg	Leu	Lys	Leu	Ala	Gln	Ile	Ile	Arg	Gln	Val	Gln	50	55	60	
Ala	Val	Phe	Pro	Phe	Phe	Arg	Glu	Asp	Tyr	Glu	Gly	Trp	Lys	Asp	Ser	65	70	75	80
Ile	Arg	His	Asn	Leu	Ser	Ser	Asn	Arg	Cys	Phe	Arg	Lys	Val	Pro	Lys	85	90	95	
Asp	Pro	Ala	Lys	Pro	Gln	Ala	Lys	Gly	Asn	Phe	Trp	Ala	Val	Asp	Val	100	105	110	
Ser	Leu	Ile	Pro	Ala	Glu	Ala	Leu	Arg	Leu	Gln	Asn	Thr	Ala	Leu	Cys	115	120	125	
Arg	Arg	Trp	Gln	Asn	Gly	Gly	Ala	Arg	Gly	Ala	Phe	Ala	Lys	Asp	Leu	130	135	140	
Gly	Pro	Tyr	Val	Leu	His	Gly	Arg	Pro	Tyr	Arg	Pro	Pro	Ser	Pro	Pro	145	150	155	160
Pro	Pro	Pro	Ser	Glu	Gly	Phe	Ser	Ile	Lys	Ser	Leu	Leu	Arg	Arg	Ser	165	170	175	
Gly	Glu	Gly	Ala	Pro	Trp	Pro	Gly	Leu	Ala	Pro	Gln	Asn	Ser	Pro	Val	180	185	190	
Pro	Ala	Gly	Thr	Gly	Asn	Asn	Gly	Glu	Glu	Ala	Val	Pro	Thr	Pro	Pro	195	200	205	
Leu	Pro	Ser	Ser	Glu	Arg	Pro	Leu	Trp	Pro	Leu	Cys	Pro	Leu	Pro	Gly	210	215	220	
Pro	Thr	Arg	Val	Glu	Gly	Glu	Thr	Val	Gln	Gly	Gly	Ala	Met	Gly	Pro	225	230	235	240
Gln	Pro	Ser	Pro	Gln	Ser	Leu	Gly	Pro	Gly	Leu	Ser	Thr	Thr	Ala	Gly	245	250	255	

His Arg Ser Ser Gly Gly Arg Ser Ser Gly Gly His Arg Ala Ser Leu  
 260 265 270  
 Trp Gly Gln Leu Pro Thr Ser Tyr Leu Pro Ile Tyr Thr Pro Asn Val  
 275 280 285  
 Val Met Pro Leu Ala Pro Pro Pro Thr Ser Cys Pro Gln Cys Pro Ser  
 290 295 300  
 Thr Ser Pro Ala Tyr Trp Gly Val Ala Pro Glu Thr Arg Gly Pro Pro  
 305 310 315 320  
 Gly Leu Leu Cys Asp Leu Asn Ala Leu Phe Gln Gly Val Pro Pro Asn  
 325 330 335  
 Lys Ser Ile Tyr Asp Val Trp Val Ser His Pro Arg Asp Leu Ala Ala  
 340 345 350  
 Pro Gly Pro Gly Trp Leu Leu Ser Trp Cys Ser Leu Glx Gly Ser Glx  
 355 360 365  
 Asp Arg Gly Arg Ser Ser Leu Pro Leu Pro Pro Pro Cys Glx Gln  
 370 375 380  
 Gly Ala Lys Ala Arg Arg Leu Ser Ala Thr Thr Ala Ala Ser Lys His  
 385 390 395 400  
 Gln Ala Ala Ala Leu Leu Gly Val His Gly Val Tyr Trp Ala Thr Pro  
 405 410 415  
 Arg Met Ala Val Ala Gln Leu Gly Thr Thr Leu Thr Leu Val Cys His  
 420 425 430  
 Ala Cys Phe Ser Tyr Thr Gln Arg Gln Asn Cys Arg Ser Arg Leu Asn  
 435 440 445  
 Leu Asn Ile Pro Ser Glx Ser Leu Phe Ser Ala His Tyr Pro Ser Ile  
 450 455 460  
 Ser His Gln Pro Ser Pro Pro Ser Arg Ala Pro Ala Gly Gly Arg Lys  
 465 470 475 480  
 Thr His Val Asp His Leu Lys Ser Cys Pro Leu Ser Leu Ser Glu Lys  
 485 490 495  
 Lys Ser Thr Phe Phe Arg Lys Pro Val Arg Glu Leu Lys Cys Pro Thr  
 500 505 510  
 Cys Pro Gly Gly Trp Gly Gly Asn His Glx Arg Asn Leu Gln Pro Phe  
 515 520 525  
 Leu Ser Ser Phe Ile Tyr Pro Lys Gly Gly Pro Val Pro Phe Pro Gln  
 530 535 540

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other
- (B) LOCATION: 1...1
- (D) OTHER INFORMATION: Human FAST-1 SID

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:



(D) OTHER INFORMATION: Mouse FAST-1 coding region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

5 ATGGCCTCGG GCTGGGACCT GGCCTCAACT TACACTCCGA CTACCCCGAG CCCCCAGTTA 60  
GCCCTGGCTC CGGCCCAGGG CTACCTCCCT TGTATGGGGC CTCGCGACAA CTCTCAGCTG 120  
AGGCCTCCAG AGGCAGAGTC TCTTTCGAAG ACCCCCAAGA GGAGGAAGAA GAGATACCTA 180  
CGGCATGACA AGCCCCCCTA CACCTACTTG GCCATGATCG CCTTGGTAAT TCAGGCCGCA 240  
CCCTTCCGCA GGCTGAAACT GGCTCAGGTC CAGGCAGTGT TCCCCTTCTT CAGGGACGAC 300  
TATGAGGGGT GGAAGGACTC CATCCGCCAC AACCTTTCCT CTAATCGGTG CTTCCATAAG 360  
10 GTGCCCAAGG ACCCTGCAAA GCCCCAGGCC AAGGGCAACT TCTGGGCGGT GGATGTTAGC 420  
CTGATTCTCTG CTGAGGCGCT GCGCCTTCAG AACACTGCCC TGTGCCGTCG ATGGCAGAAC 480  
CGGGGCACCC ACAGAGCTTT CGCCAAGGAC CTGAGCCCTT ACGTGCTCCA CGGCCAGCCT 540  
TATCAGCCAC CCAGTCCCCC ACCACCACCT AGGGAGGGTT TCAGCATCAA GTCCCTGCTA 600  
GGGGACCCTG GGAAAGAATC CACATGGCCC CAGCATCCTG GGCTCCCTGG ACAGAGCACT 660  
15 GCAGCTCAGG CAGGCACCTT GTCAAAGGGG GAAGAAGGGA TGGGCACTGG ACCCTCTAGC 720  
TCCTCTGAGA CGCTCTGTG GCCCTCTGCT TCCCTTCTCTG GGCCACAAT CATAGAGGGG 780  
GAGAGTTCCC AAGGGGAGGT AATCAGGCCT TCTCCCGTCA CCCCAGATCA AGGCTCCTGG 840  
CCCTCCACT TACTTGAGGA TTCCGCAGAT TCCAGGGGAG TGCCCAGGAG GGGGAGCAGA 900  
GCCTCCTTGT GGGGACAGCT ACCCACTTCT TACTTGCCCA TCTATACGCC CAATGTAGTA 960  
20 ATGCCCTTGG CCACACTACC GACCACCTCT TGTCCCCAGT GCCCATCTTC TGCCAGCCCA 1020  
GCTTACTGGA GCGTAGGCAC TGAATCCCAA GGGTCCCAGG ACCTGCTCTG TGATCTAGAC 1080  
TCCCTCTTCC AGGGAGTACC ACCCAACAAG AGTATCTATG ATGTGTGGGT CAGCCATCCT 1140  
AGGGACCTGG CAGCTCCTGC CCCAGGCTGG CTCCTTTCCT GGTACAGCAT GTAATATTCT 1200  
AGGGCAGAAA GGCTGTTCT CTCTCCACC CATGAATATC ATTTTGATGA ACCAGAGCTA 1260  
25 GGACGATGTC CCGACGGACA GCTTTAAAAC ACCAGCACAG CCTTGCTGAA AACCCACAGC 1320  
TTTAATTAGG TTAATCCAGA AAGGGTTGTC TCTGCTAGAT AGGGAGGTCT GGCCAATCGT 1380  
GCCAGGAGCG GAGCTCAGCC TGTAGAGTGC CTCCTCTTGA TCCTACCTTT TCAGGCCCTC 1440  
AAGCCATCCA TCTATCCATC CCTCTGTAC CATGCCTTCC TGGCTCCAGG CTGGGGGGAG 1500  
GGAGAGCCAA AAGTGGGTCT GATCTGAAGT CTTGCCCTCT CTCAAATGCC TGGGTAGAGG 1560  
30 GTAGCACCTT TCAGGGAAAG GGTTAAGAAA TGAAAGACTG GAACGGACAT AATTTTGGTG 1620  
TAATGGAAGT AGGGGAGCGA TTAATAGTAA AGGAATTTAC AACATTTT 1668

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Mouse FAST-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

45 Met Ala Ser Gly Trp Asp Leu Ala Ser Thr Tyr Thr Pro Thr Thr Pro  
1 5 10 15

5 Ser Pro Gln Leu Ala Leu Ala Pro Ala Gln Gly Tyr Leu Pro Cys Met  
 20 25 30  
 Gly Pro Arg Asp Asn Ser Gln Leu Arg Pro Pro Glu Ala Glu Ser Leu  
 35 40 45  
 10 Ser Lys Thr Pro Lys Arg Arg Lys Lys Arg Tyr Leu Arg His Asp Lys  
 50 55 60  
 Pro Pro Tyr Thr Tyr Leu Ala Met Ile Ala Leu Val Ile Gln Ala Ala  
 65 70 75 80  
 Pro Phe Arg Arg Leu Lys Leu Ala Gln Val Gln Ala Val Phe Pro Phe  
 85 90 95  
 Phe Arg Asp Asp Tyr Glu Gly Trp Lys Asp Ser Ile Arg His Asn Leu  
 100 105 110  
 Ser Ser Asn Arg Cys Phe His Lys Val Pro Lys Asp Pro Ala Lys Pro  
 115 120 125  
 15 Gln Ala Lys Gly Asn Phe Trp Ala Val Asp Val Ser Leu Ile Pro Ala  
 130 135 140  
 Glu Ala Leu Arg Leu Gln Asn Thr Ala Leu Cys Arg Arg Trp Gln Asn  
 145 150 155 160  
 Arg Gly Thr His Arg Ala Phe Ala Lys Asp Leu Ser Pro Tyr Val Leu  
 165 170 175  
 20 His Gly Gln Pro Tyr Gln Pro Pro Ser Pro Pro Pro Pro Arg Glu  
 180 185 190  
 Gly Phe Ser Ile Lys Ser Leu Leu Gly Asp Pro Gly Lys Glu Ser Thr  
 195 200 205  
 25 Trp Pro Gln His Pro Gly Leu Pro Gly Gln Ser Thr Ala Ala Gln Ala  
 210 215 220  
 Gly Thr Leu Ser Lys Gly Glu Glu Gly Met Gly Thr Gly Pro Ser Ser  
 225 230 235 240  
 Ser Ser Glu Thr Pro Leu Trp Pro Leu Cys Ser Leu Pro Gly Pro Thr  
 245 250 255  
 30 Ile Ile Glu Gly Glu Ser Ser Gln Gly Glu Val Ile Arg Pro Ser Pro  
 260 265 270  
 Val Thr Pro Asp Gln Gly Ser Trp Pro Leu His Leu Leu Glu Asp Ser  
 275 280 285  
 35 Ala Asp Ser Arg Gly Val Pro Arg Arg Gly Ser Arg Ala Ser Leu Trp  
 290 295 300  
 Gly Gln Leu Pro Thr Ser Tyr Leu Pro Ile Tyr Thr Pro Asn Val Val  
 305 310 315 320  
 Met Pro Leu Ala Thr Leu Pro Thr Thr Ser Cys Pro Gln Cys Pro Ser  
 325 330 335  
 40 Ser Ala Ser Pro Ala Tyr Trp Ser Val Gly Thr Glu Ser Gln Gly Ser  
 340 345 350  
 Gln Asp Leu Leu Cys Asp Leu Asp Ser Leu Phe Gln Gly Val Pro Pro  
 355 360 365  
 45 Asn Lys Ser Ile Tyr Asp Val Trp Val Ser His Pro Arg Asp Leu Ala  
 370 375 380  
 Ala Pro Ala Pro Gly Trp Leu Leu Ser Trp Tyr Ser Met  
 385 390 395

(2) INFORMATION FOR SEQ ID NO:18:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 88 amino acids  
 (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
(ix) FEATURE:

5 (A) NAME/KEY: Other  
(B) LOCATION: 1...1  
(D) OTHER INFORMATION: Mouse FAST-1 SID

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

10 Ser Tyr Leu Pro Ile Tyr Thr Pro Asn Val Val Met Pro Leu Ala Thr  
1 5 10 15  
Leu Pro Thr Thr Ser Cys Pro Gln Cys Pro Ser Ser Ala Ser Pro Ala  
20 25 30  
15 Tyr Trp Ser Val Gly Thr Glu Ser Gln Gly Ser Gln Asp Leu Leu Cys  
35 40 45  
Asp Leu Asp Ser Leu Phe Gln Gly Val Pro Pro Asn Lys Ser Ile Tyr  
50 55 60  
20 Asp Val Trp Val Ser His Pro Arg Asp Leu Ala Ala Pro Ala Pro Gly  
65 70 75 80  
Trp Leu Leu Ser Trp Tyr Ser Met  
85